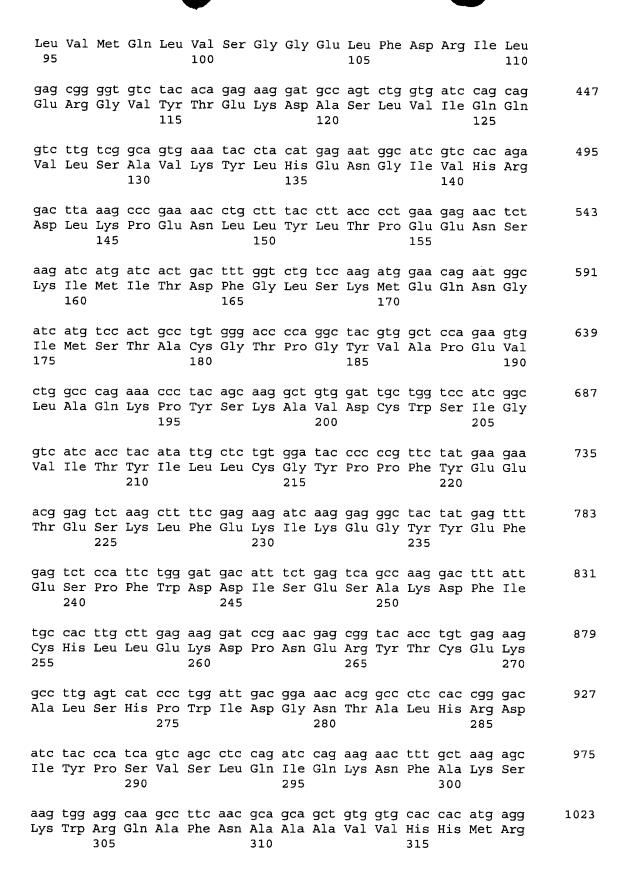
ę.

SEQUENCE LISTING

Delaney, Allen											
<120> CAMK-X1 and its Uses											
<130> KINE024											
<140> Unassigned <141> 2001-09-20											
<160> 13											
<170> FastSEQ for Windows Version 4.0											
<210> 1 <211> 2447 <212> DNA <213> H. sapiens											
<220> <221> CDS <222> (70)(1498)											
<400> 1 tggagtggga gctcaagcag gattetteee gagteeetgg cateeteaga agetteaact ctggaggca atg ggt ega aag gaa gat gae tge agt tee tgg aag aaa	60 11 1										
Met Gly Arg Lys Glu Glu Asp Asp Cys Ser Ser Trp Lys Lys 1 5 10											
	159										
1 5 10 cag acc acc aac atc cgg aaa acc ttc att ttt atg gaa gtg ctg gga Gln Thr Thr Asn Ile Arg Lys Thr Phe Ile Phe Met Glu Val Leu Gly											
cag acc acc aac atc cgg aaa acc ttc att ttt atg gaa gtg ctg gga Gln Thr Thr Asn Ile Arg Lys Thr Phe Ile Phe Met Glu Val Leu Gly 15 20 25 30 tca gga gct ttc tca gaa gtt ttc ctg gtg aag caa aga ctg act ggg Ser Gly Ala Phe Ser Glu Val Phe Leu Val Lys Gln Arg Leu Thr Gly	159										
cag acc acc aac atc cgg aaa acc ttc att ttt atg gaa gtg ctg gga Gln Thr Thr Asn Ile Arg Lys Thr Phe Ile Phe Met Glu Val Leu Gly 15 20 25 30 tca gga gct ttc tca gaa gtt ttc ctg gtg aag caa aga ctg act ggg Ser Gly Ala Phe Ser Glu Val Phe Leu Val Lys Gln Arg Leu Thr Gly 35 40 45 aag ctc ttt gct ctg aag tgc atc aag aag tca cct gcc ttc cgg gac Lys Leu Phe Ala Leu Lys Cys Ile Lys Lys Ser Pro Ala Phe Arg Asp	159 207										

ctg gtc atg cag ctt gtt tct ggt ggg gag ctc ttt gac cgg atc ctg 399



. .

aag cta cac atg aac ctg cac agc ccg ggc gtc cgc cca gag gtg gag Lys Leu His Met Asn Leu His Ser Pro Gly Val Arg Pro Glu Val Glu 320 325 330	1071
aac agg ccg cct gaa act caa gcc tca gaa acc tct aga ccc agc tccAsn Arg Pro Pro Glu Thr Gln Ala Ser Glu Thr Ser Arg Pro Ser Ser335340 345 350	1119
cct gag atc acc atc acc gag gca cct gtc ctg gac cac agt gta gca Pro Glu Ile Thr Ile Thr Glu Ala Pro Val Leu Asp His Ser Val Ala 355 360 365	1167
ctc cct gcc ctg acc caa tta ccc tgc cag cat ggc cgc cgg ccc act Leu Pro Ala Leu Thr Gln Leu Pro Cys Gln His Gly Arg Arg Pro Thr 370 375 380	1215
gcc cct ggt ggc agg tcc ctc aac tgc ctg gtc aat ggc tcc ctc cac Ala Pro Gly Gly Arg Ser Leu Asn Cys Leu Val Asn Gly Ser Leu His 385 390 395	1263
atc agc agc ctg gtg ccc atg cat cag ggg tcc ctg gcc gcc ggg Ile Ser Ser Ser Leu Val Pro Met His Gln Gly Ser Leu Ala Ala Gly 400 405 410	1311
ccc tgt ggc tgc tgc tcc agc tgc ctg aac att ggg agc aaa gga aagPro Cys Gly Cys Cys Ser Ser Cys Leu Asn Ile Gly Ser Lys Gly Lys415420	1359
tcc tcc tac tgc tct gag ccc aca ctc ctc aaa aag gcc aac aaa aaa Ser Ser Tyr Cys Ser Glu Pro Thr Leu Leu Lys Lys Ala Asn Lys Lys 435 440 445	1407
cag aac ttc aag tcg gag gtc atg gta cca gtt aaa gcc agt ggc agc Gln Asn Phe Lys Ser Glu Val Met Val Pro Val Lys Ala Ser Gly Ser 450 455 460	1455
tcc cac tgc cgg gca ggg cag act gga gtc tgt ctc att atg t Ser His Cys Arg Ala Gly Gln Thr Gly Val Cys Leu Ile Met 465 470 475	1498
gattcctgga gcctgtgcct atgtcactgc aattttcagg agacatattc aactcctctg	1558
ctcttccaaa cctggtgtct atccggcaga gggaggaagg cagagcaagt ggagcagggc	1618
ttagcaggag cagtttctgg ccagaagcac cagcctgctg ccagcggggc agcccctcat aggaggccca ggagggagcc ccaaggcgta gaagccttgt tgaagctgtg agcaggagaa	1678 1738
geggtgeeca ceagetteea ggteteeetg acetgeetge tetatgeece acaceetaeg	1798
tgccgtggct ctgtgcagtg tacgtagata gctctcgcct gggtctgtgc tgtttgtcgt	1858
gaaaagetta atgggetgge caggetgtgt caeettetee aageaaagee atatggagea	1918
tctacccaga ctcccactct gcacacactc actcccacct ctcaagcctc caacctcttg	1978 2038
gccagattgg gctcattaat gtcgttgcct gcccatctgc atgaatgaca ggcagctccc catggtggtc tgcctgtgag ctcttcaagt tctaatcctt aactccagga ttagctccca	2038
agtgcgctga gacccagcca gcacacttct ggcccttctc cctgcctcaa tctaaaagca	2158
gtgccacacc ctccaaagtg gaatagaaag aagttcatga gtaagggctg caaggaattc	2218
ttatcctggc cacatgtcct ccgtgcacac acccaatgga gttaaccttg gaagttgact	2278

attitaatgt ctgccaggag ttctaatcct gcctctgttc ccttttctct ccttgaaagt ccagcacacc attettgtcc ttccccagtt tcctcgccct ccacccctcc agettcatgc 2398 tcagtgttgt gcttaataaa atggacatat ttttctctaa aaaaaaaaa 2447

10

<210> 2 <211> 476 <212> PRT <213> H. sapiens

<400> 2

Met Gly Arg Lys Glu Glu Asp Asp Cys Ser Ser Trp Lys Lys Gln Thr Thr Asn Ile Arg Lys Thr Phe Ile Phe Met Glu Val Leu Gly Ser Gly

25 Ala Phe Ser Glu Val Phe Leu Val Lys Gln Arg Leu Thr Gly Lys Leu Phe Ala Leu Lys Cys Ile Lys Lys Ser Pro Ala Phe Arg Asp Ser Ser 55 Leu Glu Asn Glu Ile Ala Val Leu Lys Lys Ile Lys His Glu Asn Ile 75 Val Thr Leu Glu Asp Ile Tyr Glu Ser Thr Thr His Tyr Tyr Leu Val 90 85 Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Leu Glu Arg 100 105 Gly Val Tyr Thr Glu Lys Asp Ala Ser Leu Val Ile Gln Gln Val Leu 120 125 Ser Ala Val Lys Tyr Leu His Glu Asn Gly Ile Val His Arg Asp Leu 135 Lys Pro Glu Asn Leu Leu Tyr Leu Thr Pro Glu Glu Asn Ser Lys Ile 155 Met Ile Thr Asp Phe Gly Leu Ser Lys Met Glu Gln Asn Gly Ile Met 170 165 Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Leu Ala 185 Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly Val Ile 200 Thr Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Glu Glu Thr Glu 220 215 Ser Lys Leu Phe Glu Lys Ile Lys Glu Gly Tyr Tyr Glu Phe Glu Ser 235 230 Pro Phe Trp Asp Asp Ile Ser Glu Ser Ala Lys Asp Phe Ile Cys His 250 Leu Leu Glu Lys Asp Pro Asn Glu Arg Tyr Thr Cys Glu Lys Ala Leu 265 Ser His Pro Trp Ile Asp Gly Asn Thr Ala Leu His Arg Asp Ile Tyr Pro Ser Val Ser Leu Gln Ile Gln Lys Asn Phe Ala Lys Ser Lys Trp 300 295 Arg Gln Ala Phe Asn Ala Ala Ala Val Val His His Met Arg Lys Leu 315 310 His Met Asn Leu His Ser Pro Gly Val Arg Pro Glu Val Glu Asn Arg 330 325 Pro Pro Glu Thr Gln Ala Ser Glu Thr Ser Arg Pro Ser Ser Pro Glu 345 340

Ile	Thr	Ile 355	Thr	Glu	Ala	Pro	Val 360	Leu	Asp	His	Ser	Val 365	Ala	Leu	Pro		
Ala	Leu 370		Gln	Leu	Pro	Cys 375		His	Gly	Arg			Thr	Ala	Pro		
		Arg	Ser	Leu			Leu	Val	Asn		380 Ser	Leu	His	Ile	Ser		
385	_	_	_		390					395					400		
Ser	Ser	Leu	Val	Pro 405	Met	His	Gln	Gly	Ser 410	Leu	Ala	Ala	Gly	Pro 415	Cys		
Gly	Сув	Cys	Ser 420	Ser	Cys	Leu	Asn	Ile 425	Gly	Ser	Lys	Gly	Lys 430	Ser	Ser		
Tyr	Cys	Ser 435	Glu	Pro	Thr	Leu	Leu 440		Lys	Ala	Asn			Gln	Asn		
Phe	Lys 450		Glu	Val	Met			Val	Lys	Ala		445 Gly	Ser	Ser	His		
Cvs		Δla	Gly	Gln	Thr	455	V-1	Cvc	T.011	т1 о	460 Mot						
465	****	AIG	Cly	OIII	470	Gly	vai	Сув	Leu	475	Mec						
<210 <210)> 3 L> 25	5															
	2> DN																
<213	3> H.	sar	oiens	5													
<400)> 3																
gtgg	gaggg	gcg a	aggaa	acto	19 99	gaag											25
<210)> 4																
<211> 23																	
<212> DNA																	
<213	<213> Homo sapiens																
<400	> 4																
ggag	ggcg	gag g	jaaac	tggg	ıg aa	ıg										23	
<210	> 5																
<211> 25																	
<212> DNA <213> Homo sapiens																	
		/IIIO 2	apre	.11.5													
<400			<i>a</i> a	agto	~ ~~											0.5	
gugg	ayyy	icg a	ggaa	actg	9 99	aag										25	
<210																	
	> 31																
	> DN > Ho		apie	ns													
			-														
<400 ctcg		ac a	taat	gaga	c ag	actc	cagt	С								31	
				-	_		_										
<210 <211																	
	> PR																
<213	> H0	mo s	apie	ns													

<400> 7	
Lys Arg Arg Glu Ile Leu Ser Arg Arg Pro Ser Tyr Arg	
1 5 10	
<210> 8	
<211> 15	
<212> PRT	
<213> Homo sapiens	
<400> 8	
Pro Leu Ala Arg Thr Leu Ser Val Ala Gly Leu Pro Gly Lys Lys	
1 5 10 15	
<210> 9	
<211> 10	
<212> PRT	
<213> Homo sapiens	
<400> 9	
Pro Leu Ser Arg Thr Leu Ser Val Ser Ser	
1 5 10	
<210> 10	
<211> 30	
<212> DNA	
<213> Homo sapiens	
<400> 10	
gaattcaatg ggtcgaaagg aagaagatga	3 (
	5
<210> 11	
<211> 31	
<212> DNA	
<213> Homo sapiens	
<400> 11	
ctcgagtcac ataatgagac agactccagt c	
cocyagicae acaacyayae ayaccecayi c	31
<210> 12	
<211> 30	
<212> DNA	
<213> Homo sapiens	
<400> 12	
gaattcaatg ggtcgaaagg aagaagatga	30
<210> 13	
<211> 30	
<212> DNA	
<213> Homo sapiens	

ctcgagctgg atctggaggc tgactgatgg

<400> 13

30